



FIGURE 1a  
(SEQ ID NO: 1 and SEQ ID NO: 2)

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TTTAATCATG GAATATTTCA AACATACAGA AAAATCACAG AAAATAAATA ACAACCACTC ATTTATCTTC -1101
TCCCAACCC CATGTAATAA ATATTAATAA ATTGTGTTAA ATGCTAAATT TAACACATGC TAAAGCTTCC -1031
TGGCTGGATG TGGTGGCTCA CCCCTGTAAT CCCAGTACTT TGGGAGGAGG AGGTGGGAGG ATTGCTTGAG -961
TCCAGGAGCT CGAGACCAQC ATGGGCAACA TAGTGGGATC TCGTCTCTAC AAAAAACAAA AAAATTAGCT -891
GGGATGGTG CTCTGCATCA GTAATCCCAG TCACTGGGAG GCTCAGGTGG GAGAATTGCT TGAGTCTGGG -821
AATTTGAGGC TGCAGTGACC CCTGATCATG CCACTGCATT CCAGCATGGG CGACATAGCA AAACCTGTCA -751
AAAAAAAAA AAGTTTCCTC TCTGCCCCAC CATAGACAAC CACTCTCTCG ATTTCTATCT TCGTAGATGA -681
API
ATTTGCCCCA TTCTCTTCTA TATGAAAGGA ACCAGACATT AGGCATTCTG GTCTCTCGTT TCTTTCACCT -611
AAGATAAAT TGAGTTAACC TGTATTGTTG TACAGAACTG CAGTTTGTTC TTGTTATTT ATTGTAAGA -541
CAGGTCTGG CTATGTTGCC TAGGCTGGTC TCGAAGTGT GGCCTCAAGC AATCCACCTG CCAAGCTCTG -471
GGACCAAGG CATGAGCCAT GGCATCTGAT CKGTAGTTTG ATCTTATTTT TTGCTGACTA GTAGCCCATG -401
API
GCATGACTTT ATTATTTTGG GTGTCCATTC TCCTCTGGAG GGGCTCTGCT TTTTGAAGCC ACACCCCTGGC -311
Ets
CTAGCTCCCC TTCTCCCTGC CTCTCTGCAG GCTCACATCC ACATGCCAAG ACCTCTGCAG CCATTCTGCT -261
Ets
TCCTCTCTCT CCACCTCTGT GGGACCTCAG AGAGCTACGG GGCTCCCTGG GTACCAACTG GCTCCTGAGG -191
Sp1/Sp3 Sp1/Sp3
CCTGCGCGAG GGTGGTCTTC TGGGAGAAGG AAGCCAGGTC CCTGCAGGTT GTGGAGGGGG ACAGAATGAG -121
Sp1/Sp3 ETS
GGTTTTTCCC CAGGATGTTG TTGGCCCTG CCCCCACTTC TGTTCCATAA TTAACCAGCC CCTTCTACC -51
Sp1/Sp3 +1
CACTGTGCCC CTCTTCTCTG TGTGTGGAGG CCTGAATCA TTATTTTAAC TACCCCTCTG GAGGGTGAGC 20
Ets Ets
ACCTTCTGTG CTCTGTCCCC AACCTTCCAC TTCCCTCAA CGCGCTGCTC AGGGATGACC TTCGGCACTG 90
M T F G T
TGCTTCTTCT GAGTGgtang tggggccagg gtgctgggga gaagcttggg ggagttctga ggggactcca 160
V L L L S
tctgggaggg caggctgggg gctgggtggt ggctccaaac actcttatga ggagctgagg caggggagtg 230
cttcatgtgc gagtggcccg gagtcaagtag agtgtgacct gaatgaagag gggctcaggg gctgtgctca 300
gggtggcact aagctacctc tccagctgyc tatgtgtgct caggcttccc tgcctccact catggagtc 370
ctggtgtggg tgacagaggt ctecccgagc tccccgggga gtggaaggcc acagaagcca ccagggaggg 440
ggaaagggtg gacatcacct cctggggcct nnnnntccc ccaagtcctg actgcacgta gggaaagagcc 510
INTRON 1
ccccgtctga aaactgcacg agagtcacat tcacgtgcca tcaaaaaatca ggcttggctg ggtgcggtgg 580
ctcatgctta taatccagc actttgggag gccgagatgg gcgtatcccc tgaggtcagg agtttgtgac 650
cagctggcc aacatggtga aacccatct ttacaaaaaa tataaaaaatt agccgggcat ggtggcgctg 720
acttgtaac cagctactt gggaaagctga ggcaagagaa tgccttgaaac ccaggagacg gaagttgcag 790
tgagctgaga tctgcccgtt gcactccagc ctacgcaaca gagcgagact ccactctcaa aaaaaaaaaa 860
aaaaaangaa aaaaaagaaa aagaggtctg gaggtcctag ggattggggc tctcttaact cccagcctcc 930
ccgcccccca aatatctctc agTCCTGGCT TCTTATCATG GATTCACCT CGATCTGCAG GAGCCTACGA 1000
V L A S Y H G F N L D V E E P T

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**FIGURE 1b**  
(SEQ ID NO: 1 and SEQ ID NO: 2)

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TCTTCCAGGA GGATGCAGGC GGCTTTGGGC AGAGCGTGGT GCAGTTGGGT GGATCTCGgt agggcccact 1070
I F Q E D A G G F G Q S V V Q F G G S R
-----INTRON 2 (3019 bp)-----
cccccaagtg cccgctgctc ccacccctcc tctggtctga gtgacatggc catggttggt tctccagACT 4080
L
CGTGGTGGGA GCACCCCTGG ACCTGGTGGC GGGCAACCAG ACGGGACGGC TGTATCACTG CCCAGCTGCC 4150
V V G A P L E V V A A N Q T G R L Y D C A A A
ACCGGCATGT GCCAGCCCAT CCCGCTGCAC Agtgagtgac cactgggaa ttgggcccct caacccctct 4220
T G M C Q P I P L H INTRON 3
ggacccaact gtgccccgc tttagcttcca gtccagacct tccccgcmaa tyagtgtgtg ctgtgagtga 4290
gaaccccggt gtctgcccct gcaTCCGCC CTCAGGCCGT GAACATGTTC TTGGCCCTGA CCCTGGCAGC 4360
I R P E A V N M S L G L T L A A
CTCCACCAAC GGCTCCCGGC TCCTGgtgag tgagtgtctt gggccacggg ggggtgggt gggggggggg 4430
S T N G S R L L INTRON 4
gtgtgtgttg ggaggaggt ggggtggga gtgaaggagg aggggtgtgt agggactcct ggctcacagg 4500
cttctgcctc cagGCCCTGTG GCGCCACCT CCACAGAGTC TGTGGGAGA ACTCATACTC AAAGGGTTCC 4570
A C G P T L H R V C G E N S Y S K G S
TGCTCTCTGC TGGCTCCCG CTCGGAGATC ATCCAGACAG TCCCCGAGC CAGCCAGgt aggtccctgg 4640
C L L L G S R W E I I Q T V P D A T P
-----INTRON 5 (4267 bp)-----
caggagctgc aggaggggt tgggccccg cagtgcctc ccgattcctc cccattcccc cagagAGTGT 8840
E C
CCACATCAAG AGATGGACAT CGTCTTCTG ATTGACGGCT CTGGAAGCAT TGACCAAAAT CACTTTAACC 8910
P H Q E M D I V F L I D G S G S I D Q N D F N
AGATCAAGGG CTTGTCCAA GCTGTCATGG GCCAGTTGA GGGCACTGAC ACCCTGgtga agactgggca 8980
Q M K G F V Q A V M G Q F E G T D T L
-----INTRON 6 (1255 bp)-----
aacaatagta acaggcactg agccctgggc cctccccact ggcctttgca gTTGCACTG ATGCAGTACT 10240
P A L M Q Y
CAAACCTCCT GAAGATCCAC TTCACCTTCA CCCAATTCCG GACCAGCCCG AGCCAGCAGA GCCTGGTGGA 10310
S N L L K I H F T F T Q F R T S P S Q Q S L V D
TCCCATCGTC CAACTGAAAG GCCTGACGTT CAGGGCCAGC GGCATCCTGA CACTGGTgt aagcaacccc 10380
P I V Q L K G L T F T A T G I L T V
gacccca-----INTRON 7

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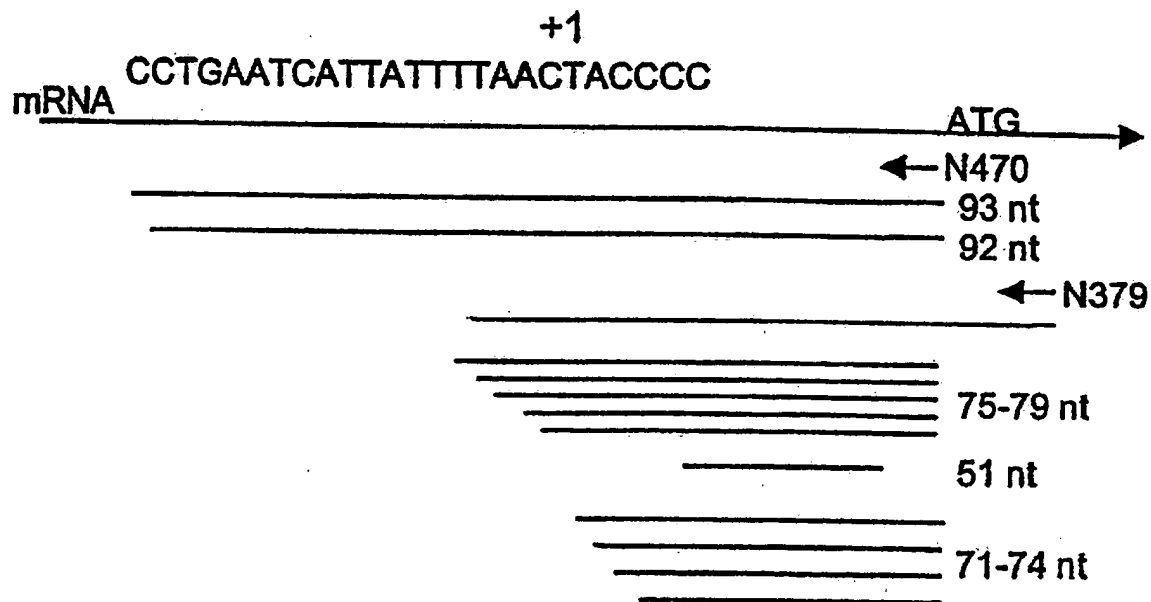
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## FIGURE 3

SEQ ID NO: 4 (Also positions 1152 to 1176 of SEQ ID NO: 1)





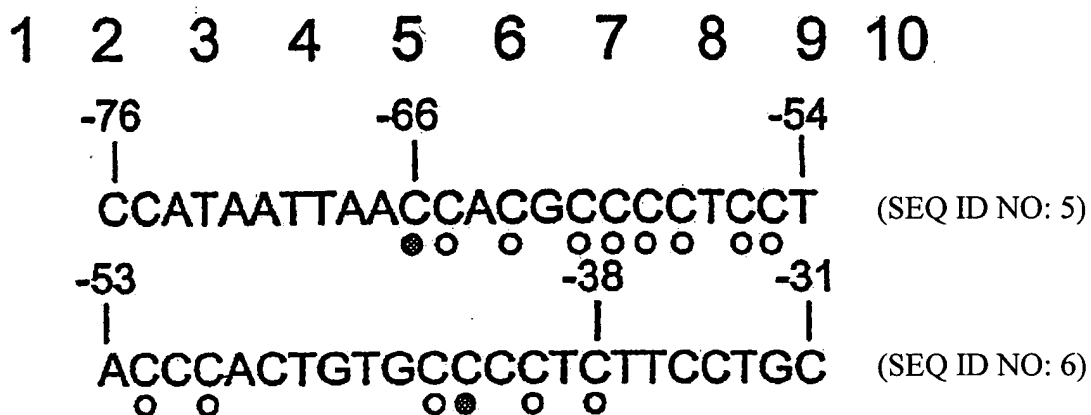
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## FIGURE 8

SEQ ID NOS: 5 and 6  
(SEQ ID NOS: 5 and 6 are collectively  
positions 1095 to 1140 of SEQ ID NO: 1)



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Sequence Range: -11390 to 10387  
(SEQ ID NO:3)

### FIGURE 9

Protein Sequence: SEQ ID NO:2

### Translational stop codon for CD11c

-11321

TGATCCCTCT TTGCCTTGA CTTCTTCTCC CGCGATTTTC CCCACTTACT TACCCTCACC TGTCAGGCTG

ACGGGGAGGA ACCACTGCAC CACCGAGAGA GGCTGGGATG GGCCTGCTTC CTGTCTTTGG GAGAAAACGT -11251

CTTGCTTGGG AAGGGGCCTT TGTCTTGTC AAGTTCCAAC TGGAAACCTT TAGGACAGGG TCCCTGCTGT -11181

GTTCCTCCAAA AGGACTTGAC TTCGAATTC TACCTAGAAA TACATGGACA ATACCCCCAG GCCTCAGTCT -11111

CCCTTCTCCC ATGAGGCACG AATGATCTTT CTTTCCTTTC CTTTTTTTTT TTTTCTTTT CTTTTTTTTT -11041

TTTTTTGAGA CGGAGTCTCG CTCTGTCACC CAGGCTGGAG TGCAATGGCG TGATCTCGGC TCGCTGCAAC -10971

CTCCGCCTCC CGGGTTCAAG TAATTCTGCT GTCTCAGCCT CCTGCGTAGC TGGGACTACA GGCACACGCC -10901

ACCTCGCCCG GCCCGATCTT TCTAAAATAC AGTTCTGAAT ATGCTGCTCA TCCCCACCTG TCTTCAACAG -10831

CTCCCCATTA CCCTCAGGAC AATGTCTGAA CTCTCCAGCT TCGCGTGAGA AGTCCCCTTC CATCCCAGAG -10761

GGTGGGCTTC AGGGCGCACA GCATGAGAGC CTCTGTGCCC CCATCACCCCT CGTTTCCAGT GAATTAGTGT -10691

-10621

CATGTCAGCA TCAGCTCAGG GCTTCATCGT GGGGCTCTCA GTTCCGATTC CCCAGGCTGA ATTGGGAGTG

-10551

AGATGCCTGC ATGCTGGGTT CTGCACAGCT GGCCTCCCGC GGTTGGGTCA ACATTGCTGG CCTGGAAGGG

-10481

AGGAGCGCCC TCTAGGGAGG GACATGGCCC CGGTGCGGCT GCAGCTCACC AGCCCCAGGG GCAGAAGAGA

CCCAACCACT TCCTATTTTT TGAGGCTATG AATATAGTAC CTGAAAAAAT GCCAAGCACT AGATTATTTTT

TTTAAAAAGC GTACTTTAAA TGTGTGTGT AATACACATT AAAACATGCA CAAAAAGATG CATCTACCGC

-10271

TCTTGGGAAA TATGTCAAAG GGTCTAAAAA TAAAAAAGCC TTCTGTGGAT ATGAGTCCTG AAGGATGACA

CCCATGGGGT CCCTTTACCA CGGTGGACCC TGGCCAGCAC TGAGGCCTGG GGCCAGGACA AGAAGTTAAC -10201

-10131

CAGAGTAGGG TTGTGAATAT CCCTCTCTTG GAAGTAACCT GACCTCTTAA TCTGCTCACT CCACCTCTCAG

-10061